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#### SEQUENCE LISTING

### (1) GENERAL INFORMATION:

5 (i) APPLICANT: (A) NAME: BRIGHAM AND WOMEN'S HOSPITAL (B) STREET: \\$5 FRANCIS STREET (C) CITY: BOSTON (D) STATE: MASSACHUSETTS 10 (E) COUNTRY: USA (F) POSTAL CODE \((ZIP): 02115 (A) NAME: DANA-FARBER CANCER INSTITUTE (B) STREET: 44 BINNEY STREET (C) CITY: BOSTON 15 (D) STATE: MASSACHUSETTS (E) COUNTRY: USA (F) POSTAL CODE (ZIP): 02115

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules and Uses Therefor

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 60 State Street \ suite 510

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/205,697

(B) FILING DATE: 02-Mar-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.

(B) REGISTRATION NUMBER: 36,207

(C) REFERENCE/DOCKET NUMBER: BWI-120CPPC

(ix) TELECOMMUNICATION INFORMATION:

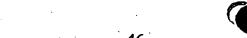
(A) TELEPHONE: (617)227-7400

(B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1888 base pairs



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	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
<i>.</i> ; .	(D) TOPOLOGY linear
· ·	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
3	(ii) MOLECULE TYPE: CDNA
	\
-	(ix) FEATURE:
	1
10	(A) NAME/KEY: CDS
10	(B) LOCATION: 249.\.1208
	(xi) SEQUENCE DESCRIPTION: SEO
	(XI) SEQUENCE DESCRIPTION:\SEQ

### ID NO:1:

	(XI) SEQUENCE DESCRIPTION:\SEQ ID NO:1:	
15	GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC	60
	TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
20	TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA	180
	GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT	240
25	CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC  Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  1 5 10	290
30	AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30	338
<u>-</u>	CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val  35 40 45	386
35	AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp 50 55 60	434
40	GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu 65 70 75	482
45	TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg 80 85 90	530
50	ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val 100 105 110	578
	CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg 115 120 125	626
55	GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys 130	674 <sup>-</sup>



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	GCT Ala	GAC Asp	Phe	Ser	ACC Thr	Pro	AAC \Asn	ATA Ile 150	Thr	GAG Glu	TCT Ser	GGA Gly	AAC Asr 155	Pro	TCT	GCA Ala	_	722
: <b>5</b>	GAC Asp	ACT Thr	AAA Lys	AGG Arg	ATT Ile	ACC Thr	TGC Cys 165	TTT	GCT Ala	TCC Ser	GGG	GGT Gly 170	TTC Phe	CCA Pro	AAG Lys	CCT Pro		770
10	CGC Arg 175	Phe	TCT Ser	TGG Trp	TTG Leu	GAA Glu 180	AAT Asn	GGA Gly	AGA Arg	GAA Glu	TTA Leu 185	CCT Pro	GGC Gly	ATC Ile	AAT Asn	ACG Thr 190		818
15	ACA Thr	ATT	TCC Ser	CAG Gln	GAT Asp 195	CCT Pro	GAA Glu	TCT Ser	GAA Glu	TTG Leu 200	TAC Tyr	ACC Thr	ATT Ile	AGT Ser	AGC Ser 205	CAA Gln		866
20	CTA Leu	GAT Asp	TTC Phe	AAT Asn 210	ACG Thr	ACT Thr	CGC Arg	AAC Asn	CAC His 215	ACC Thr	ATT Ile	AAG Lys	TGT Cys	CTC Leu 220	ATT Ile	AAA Lys		914
20	TAT Tyr	GGA Gly	GAT Asp 225	GCT Ala	CAC His	GTG Val	TCA Ser	GAG Glu 230	GAC Asp	TTC Phe	ACC Thr	TGG Trp	GAA Glu 235	AAA Lys	CCC Pro	CCA Pro		962
25	GAA Glu	GAC Asp 240	CCT Pro	CCT Pro	GAT Asp	AGC Ser	AAG Lys 245	AAC Asn	ACA Thr	CTT Leu	GTG Val	CTC Leu 250	TTT Phe	GGG Gly	GCA Ala	GGA Gly		1010
30	TTC Phe 255	GGC Gly	GCA Ala	GTA Val	ATA Ile	ACA Thr 260	GTC Val	GTC Val	GTC Val	ATC Ile	GTT Val 265	GTC Val	ATC Ile	ATC Ile	AAA Lys	TGC Cys 270		1058
35	TTC Phe	TGT Cys	AAG Lys	CAC His	GGT Gly 275	CTC Leu	ATC Ile	TAC Tyr	CAT His	TTG Leu 280	CAA Gln	CTG Leu	ACC Thr	TCT Ser	TCT Ser 285	GCA Ala		1106
40	AAG Lys	GAC Asp	TTC Phe	AGA Arg 290	AAC Asn	CTA Leu	GCA Ala	Leu	CCC Pro 295	$\mathtt{Trp}$	CTC Leu	TGC Cys	AAA Lys	CAC His	GGT Gly	TCT Ser		1154
40	CTA Leu.	GGT Gly	GAA Glu 305	GCC Ala	TCT Ser	GCA Ala	Val	ATT Ile 310	TGC Cys	AGA Arg	AGT Ser	Thr	CAG Gln 315	ACG Thr	AAT Asn	GAA Glu	•	1202
45	Pro	CAG Gln 320	TAGT	TCTG	CT G	TTTC	TGAG	g ac	GTAG	TTTA	GAG.	ACTG.	AAT	TCTT	TGGA	ÅA \		1258
50	GGAC	ATAG	GG A	CAGT	TTGC	A CA	TTTG	CTTG	CAC	ATCA	CAC :	ACAC	ACAC	AC A	CACA	CACAC		1318
∵	ACAC	ACAC	AC A	CACA	CACA	C AC	ACAC	ACAC	ACA	CACA	CAC '	TCTC'	rctc	TC T	CTCT	CTCTC		1378
	GATA	CCTT	AG G	ATAG	GGTT	C TA	CCCT	<b>FTT</b> G	CTC	AGTG.	ACA Z	AAGA	ATCA	CT C	rgtg(	GCGGA		1438
55																TCCAG	Ţ	1498
																TCCAA		1558
	GAGG	GAAC	CT G	AATT	ATGA	A GG	rgagi	rcag	AAT	CCAG	ATT :	rccto	GCT	CT A	CCAC'	TCTTA	, ,	1618



	AC	CTGT	ATCT	GTT.	AGAC	ccc i	AAGC:	rętg:	AG C	TCAT	AGAC	: A AG	CTAA	TTTA	AAA	TGCT	PTT
5	TA	ATAA	GCAG	AAG	GCTC1	AGT 1	ragt <i>i</i>	ACGG(	GG T	TCAG	GATA	C TG	CTTA	CTGG	CAA	TATT	<b>rga</b>
J	CT.	AGCC'	TCTA	TTT.	rgtt:	rgt :	rttt	/ AAA1	G C	CTAC	TGAC'	r gt	AGTG'	TAAT	TTG	TAGG	AAA
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15	(2)	INI		ATION													
13	•		(i)	(E	JENCE L) LE B) TY D) TO	NGTH PE:	: 32 amin	0 am	ino id		is						
20		(	(ii)	MOLE	CULE	TYP	E: p	rote	in								
		(	(xi)	SEQU	ENCE	DES	CRIP	TION	: SI	EQ II	) 0 NO:	2:					
25 1	Met 1	Ala	Cys	a Asn	Cys 5	Gln	Leu	Met	Glr	Asp 10		Pro	Leu	ı Leu	Lys 15	Phe	
\	Pro	Cys	Pro	Arg 20	Leu	Asn	Leu	Leu	Phe 25	Val	Leu	Leu	\le	Arg		Ser	
30	Gln	Val	Ser 35	Ser	Asp	Val	Asp	Glu 40	Gln	Leu	Ser	Lys	Ser	Val	.Lys	Asp	
35	Lys	Val 50	Leu	Leu	Pro	Cys	Arg 55	Tyr	Asn	Ser	Pro	His 60	Glu	Asp	Glu	Ser	
	Glu 65	Asp	Arg	Ile	Tyr	Trp 70	Gln	Lys	His	Asp	Lys 75	Val	Val	Leu	Ser	Val 80	
10	Ile	Ala	Gly	Lys	Leu 85	Lys	Val	Trp	Pro	Glu 90	Tyr	Lys	Asn	Arg	Thr 95		
-				Thr 100					105					110	,	\	
5			115	Thr				120					125				
0		130	-	Lys			135				-	140				\	
	Phe 145	Ser	Thr	Pro	Asn	Ile -150	Thr	Glu	Ser	Gly	Asn 155	Pro	Ser	Ala	Asp	Thr 160	
5	Lys	Arg	Ile	Thr	Cys 165	Phe	Ala	Ser	Gly	Gly 170	Phe	Pro	Lys	Pro	Arg 175	Phe	
	Ser	Trp	Leu	Glu 180	Asn	Gly	Arg	Glu	Leu 185	Pro	Gly	Ile ·	Asn	Thr 190	Thr	Ile	

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	Ser	Gln	Asp 195	Pro	Glu	Ser	Glu	Leu 200	Tyr	Thr	:Ile	Ser	Ser 205	Gln	Leu	Asp	÷	
5	Phe	Asn 210	Thr	Thr	Arg	Asn	His 215	Thr	Ile	Lys	Cys	Leu 220	Ile	Lys	Tyr	Gly		
	<b>A</b> sp 225	Ala	His	Val	Ser	Glu 230	Asp	Phe	Thr	Trp	Glu 235	Lys	Pro	Pro	Glu	Asp 240		
10	Pro	Pro	Asp	Ser	Lys 245	Asn	Thr	Leu	Val	Leu 250	Phe	Gly	Ala	Gly	Phe 255	Gly		
15	Ala	Val	Ile	Thr 260	Val	Val	Val	Ile	Val 265	Val	Ile	Ile	Lys	Cys 270	Phe	Cys		
13	Lys	His	Gly 275	Leu	Ile	Tyr	His	Leu 280	Gln	Leu	Thr	Ser	Ser 285	Ala	Lys	Asp		
20	Phe	Arg 290	Asn	Leu	Ala	Leu	Pro 295	Trp	Leu	Cys	Lys	His 300	Gly	Ser	Leu	Gly		
	Glu 305	Ala	Ser	Ala	Val	Ile 310	Cys	Arg	Ser	Thr	Gln 315	Thr	Asn	Glu	Pro	Gln 320		٠
25	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:3:			\							
b \ 30		(i)	(A (E (C	L) LE S) TY S) ST	NGTH PE: RAND	IARAC I: 25 nucl EDNE	16 b eic SS:	ase acid doub	pair l	·s		-\	\					٠
35		(ii)	MOL	ECUL	E TY	PE:	CDNA	•						\				
40		(ix)		.) NA	ME/K	EY: ON:		.116	6									
		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:3:							
45	GAGT	TTTA	TA C	CTCA	ATAG	A CT	CTTA	.CTAG	TTT	CTCT	TTT	TCAG	GTTG	TG A	AACŢ	CAACO	C	60
	TTCA	AAGA	CA C	TCTG	TTCC	А ТТ	TCTG	TGGA	CTA	ATAG	GAT	CATC	TTTA	GC A	TCTG	cccc	3	120
	TGGA	TGCC	AT C	CAGG	CTTC	т тт	TTCT	ACAT	CTC	TGTT	TCT	CGAT	TTTT	GT G	AGCC'	TA <b>Ç</b> GA	Ą	180
50	GGTG	CCTA	AG C	TCCA	TTGG	C TC	TAGA	TTCC	TGG	CTTT	CCC	CATC	ATGT	TC T	CCAA	AGCĄT	Γ.	240
	CTGA	AGCT	ATG Met 1	Ala	TGC Cys	AAT Asn	TGT Cys 5	Gln	TTG Leu	ATG Met	CAG Gln	GAT Asp	Thr	CCA Pro	CTC Leu	CTC Leu		290
55 -	AAG 1 Lys 1	TTT (	CCA '	TGT (	CCA . Pro .	AGG ( Arg 20	CTC .	AAT (	CTT ( Leu :	CTC ! Leu !	TTT ( Phe '	GTG (	CTG (	CTG 1	AAT ( Asn <i>l</i>	CGT Arg 30		338

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	CT: Le	T TC u Se	A CA r Gl:	A GT( n Val	TC' Se:	r Sei	A GAT	r GT O Va	T GA	p Gl	A CA u Gl o	A CT	G TC u Se	C AA r Ly	G TC S Se 4	r Va	386 1
5	AA) Lys	A GA	T AAC p Ly:	G GTA s Val	L Le	G CTO	G CCT	r TG	C CG' S Arg	g Ty	C AA	C TC' n Se:	T CC r Pr	T CA O Hi 6	s Gl	A GA:	Г 434 Э
10	GA0 Glu	TC:	T GAM r Glu 65	A GAC 1 Asp	C CGA	A ATO	TAC Tyr	TGC Trp	ο <b>G</b> γί	A AA	A CA'	T GAG	C AA p Ly: 7!	s Vai	G GTG	G CTO	G 482
15	TC1 Ser	GT( Va]	r TTE	GCT Ala	GGG Gly	AAA Lys	CTA Leu 85	Lys	A GTO	G TGC	G CCC	GAC Glu	туз	r AA(	G AA( s Ası	C CGG	530
20	ACT Thr 95	ьес	A TAI	GAC Asp	AAC Asn	ACT Thr	Thr	TAC	TCI Ser	CTT Lev	114 105	: Ile	CTC	GGG GGI	CTC / Lev	GTC Val	
	CTT Leu	TCA Ser	A GAC	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	Val	. Val	CAA Gln	AAG Lys	AAG Lys	GAA Glu 125	Arg	626
25	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	Leu	GTA Val	AAG Lys	TTG	TCC Ser	Ile	AAA Lys	674
30	GCT Ala	GAC Asp	TTC Phe 145	TCT Ser	ACC Thr	CCC Pro	AAC Asn	ATA Ile 150	ACT Thr	GAG Glu	TCT Ser	GGA Gly	AAC Asn 155	Ρŗο	TCT Ser	GCA Ala	722
35	GAC Asp	ACT Thr 160	AAA Lys	ÄGG Arg	ATT Ile	ACC Thr	TGC Cys 165	TTT Phe	GCT Ala	TCC Ser	GGG Gly	GGT Gly 170	TTC Phe	CCA Pro	AAG Lys	CCT Pro	770
40	CGC Arg 175	TTC Phe	TCT Ser	TGG Trp	TTG Leu	GAA Glu 180	AAT Asn	GGA Gly	AGA Arg	GAA Glu	TTA Leu 185	CCT Pro	GGC Gly	ATC Ile	AAT Asn	ACG Thr 190	818
	ACA Thr	ATT Ile	TCC Ser	CAG Gln	GAT Asp 195	CCT Pro	GAA Glu	TCT Ser	GAA Glu	TTG Leu 200	TAC Tyr	ACC Thr	ATT Ile	AGT Ser	AGC Ser 205	CAA Gln	866
45	CTA Leu	GAT Asp	TTC Phe	AAT Asn 210	ACG Thr	ACT Thr	CGC Arg	AAC Asn	CAC His 215	ACC Thr	ATT Ile	AAG Lys	TGT Cys	CTC Leu 220	ATT Ile	AAA Lys	914
50	TYL	С1У	225		HIS	Val	Ser	Glu 230	Asp	Phe	Thr	Trp	Glu 235	Lys	Pro	Pro	962
55		240	PEO.	PIO .	Asp	ser	Lys . 245	Asn	Thr	Leu	Val	Leu 250	Phe	Gly	Ala	Gly	1010
	Phe 255	GGC Gly	GCA Ala	GTA . Val	тте	ACA Thr 260	GTC ( Val	GTC Val	GTC Val	Ile	GTT Val 265	GTC Val	ATC Ile	ATC Ile	Lys	TGC Cys 270	1058

5	TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu 275 280 285	1106
J	ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln 290 300	1154
10	ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG Thr Val Phe Leu 305	1206
15	GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	1266
	ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1326
	CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1386
20	ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1446
	GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1506
25	GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG	1566
	GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGGGA GGGAGGGGA CGGGGTGGGG	1626
	GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG	1686
0	AGAGTATTGA GCGGTCTCAT CTACCATTTG CAACTGACCT CTTCTGCAAA GGACTTCAGA	1746
<u> </u>	AACCTAGCAC TACCCTGGCT CTGCAAACAC GGTTCTCTAG GTGAAGCCTC TGCAGTGATT	1806
5	TGCAGAAGTA CTCAGACGAA TGAACCACAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA	1866
	GAGACTGAAT TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC	1926
	ACACACACA ACACACACA ACACACACA ACACACACA	1986
0	TCTCTCTCTC TCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA	2046
	AAGAATCACT CTGTGGCGGA GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT	2106
5	CCTGAGTGCC AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA	2166
	TGAAGACACT GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT	2226
	TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA	2286
	AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC	2346
	TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTTTGT TTTTTAAAGG CCTACTGACT	240.6
;	GTAGTGTAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT	2466
	TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT	2516

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 818 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: cDNA  (ix) FEATURE:	
	(A) NAME/KEY: CDS (B) LOCATION: 1138	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	<u>-</u>
20	GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg  1 5 10 15	48
25	AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala 20 25 30	96
	TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA CCA CAG Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln 35 40 45	138
30	TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA GGACATAGGG	198
	ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACA ACACACACA ACACACAC	258
b <sup>35</sup>	ACACACACA ACACACACA ACACACACA TCTCTCTCT TCTCTCTC	318
á	GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC	378
40	AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA	438
40	TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT	498
	GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT	558
45	GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG	618
	AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA CTAGCCTCTA	678
50	TTTTGTTTGT TTTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA CATGTTGCTA	738
50	TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC TTTCCAGGTA	798
	TTTCCCTTTT TATCCTTCAT	818
55	(2) INFORMATION FOR SEQ ID NO:5:	-

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: amino acid

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## (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

•	(xi)	SEQUENCE	DESCRIPT	ţON:	SEQ	ID	NO:5
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Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg

1 10 15

Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala 20 25 30

Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
35 40 45

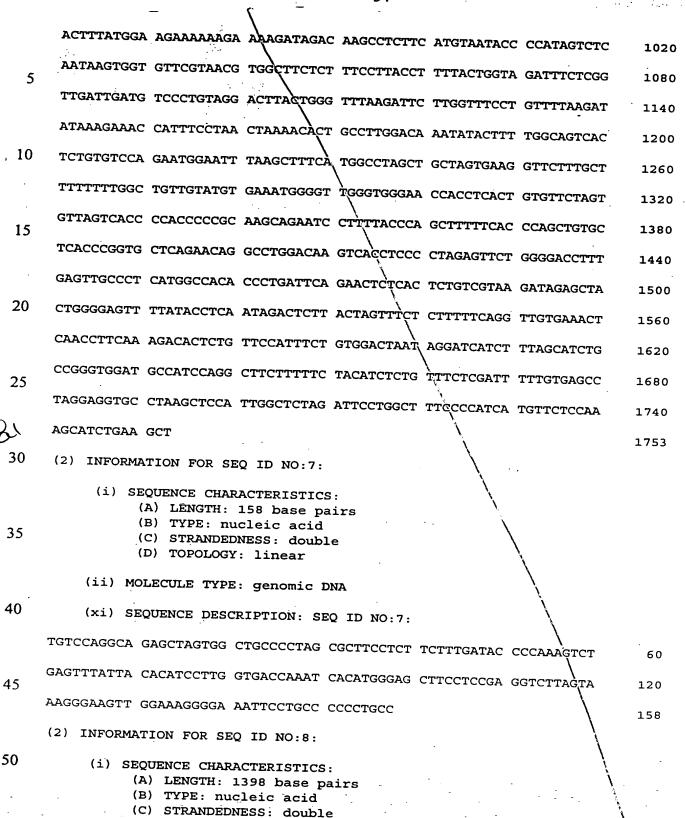
## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTTTAGTAA CCAGAGGCCG CAAGAAGAGA TCACTTGTAT ATACACGGGC CCCATCTTTT 60 GCTTTTTAAG ACAAAAGAAA AAGAATCTTC TTCAACAAGT AAGTAAATGC ATTTACTATT 120 TATCATGCTA TGGGACACCT TAGTAGAACA CGCTATCTCC AGCCTTATCA TATGCATATT 180 TTGTTGTTGT TGTTGTTGTT GTTGTTAAAG ACAGGGTCTC ATATATGCCA GGCTGGTCCC 240 AAACTTTCAG TGTAACCCAA GATAATCTGG AACTCCCGAC TCCTCTGCTC, CCACCTCTCC 300 AGTGCAGGAC ACTGTTTATA CCGTGCTGGG GAATTGAACT CAGAGCACCC  $^{\eta}$ CGCATGTCAG 360 CTAAGCATTC TACCGACCAA GTCCCATGCC CAGTCCCTAA CTCCCCAACT TCACTGCTTT 420 TTAAACATAC ATACAATCAT AACTTGCCCT CAGAGCAGTC TCCTGGGGTC TCTTATTCTC 480 AAGGCTGCGG CATTCCAACA CTGTTAGAAA AACACCATCA GGATTCTTTT GTGTT $^{\mathbb{N}}$ CCTA 540 GATGCAAACA TTTTTGTAGG GCGAAGTTGA GGTTTTTCTA ATCAAGAAAA TGCCGGTAAC 600 AAGTCTCTTC AAGCTAACTG GTTGGCTAAG GGGTATCTCT CCAAAAGAAG AGATCCACAT 660 GTCAGGCCAG TTGTAGGCAT GATGTCAGGT CTCCCTCCCT TTCTTTCTTT CTTTCTTTTT 720 780 GGTTTTTCGA GACAGGGTTT CTTTGTATAG CCCTGGCTGT CCTGGAACTC GCTCTGTAGA 840 CCAGGCTGGC CTCGAACTCA GAAATCTGCC TCTGCCTTTA CCTCCTGAGT GCTGGGAATT 900 AAAGGTGTGC ACCACCATGC CCGGCTGGGA TGTCATTCGT TTTCATTTCT CAATTTTGAT 960



(ii) MOLECULE TYPE: cDNA

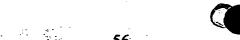
(ix) FEATURE:

(A) NAME/KEY: CDS

(D) TOPOLOGY: linear

### (B) LOCATION: 249..848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: 5 GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC 60 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 10 180 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290 15 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 20 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG 386 Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 40 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC 434 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys, Phe Ala Ser 55 GGG GGT TTC CCA AAG CCT CGC TTC TCT TGG TGG GAA AAT GGA AGA GAA Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Trp Glu Asn Gly Arg Glu 482 65 TTA CCT GGC ATC AAT ACG ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG 530 35 Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu 80 TAC ACC ATT AGT AGC CAA CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC 578 Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr 40 95 ATT AAG TGT CTC ATT AAA TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC 626 Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe 45 ACC TGG GAA AAA CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT 674 Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu 50 GTG CTC TTT GGG GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC 722 Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile 145 150 GTT GTC ATC AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA 77Ò Val Val Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg 160



	AAT GAG GCA AGC AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu 175 180 185 190	818
5	GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT Glu Ala Leu Ala Glu Gln Thr Val Phe Leu 195 200	868
10	GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT	928
	GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG	988
	GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT	1048
15	GAAGTGGAAA GGCTGAGCCC ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC	1108
	TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT	1168
20	TGATATGTCA TGTTTGGTTG GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT	1228
	GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA	1288
	GGGAGGGGA CGGGTGGGG GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA	1348
25	TATAAATATT AAATAAAAA AGAGTATTGA GCAAAAAAAA AAAAAAAAA	1398
	(2) INFORMATION FOR SEQ ID NO:9:	
30	(i) SEQUENCE CHARACTERISTICS:	-
ubal	(A) LENGTH: 200 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
40	Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  1 5 10 15	
	Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser 20 25 30	
45	Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly 35 40 45	
50	Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly 50 55 60	`\
	Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro 65 70 75 80	
55	Gly Tie Asp Thr The Con Gly No. 7	1
	Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr 85 90 95  Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys	Ĭ,

	Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp 115 120 125	
5	Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu 130 135 140	
	Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val 145 150 160	
10	Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu 165 170 175	
15	Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala 180 185 190	
	Leu Ala Glu Gln Thr Val Phe Leu 195 200	
20	(2) INFORMATION FOR SEQ ID NO:10:	
0.5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 1570 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
25	(ii) MOLECULE TYPE: cDNA	
20		
30 b	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 249890	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	\	50
40		20
	TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 16	30
45	GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT  CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC  24	
	Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  1 5 10	10
50	AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  20 25 30	8
55	CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 35 40 45	6
	TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser 50 55 60	4

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	3	1	65		Lys	- 10	mg	70	ser	пр	Leu	GIU	Asn 75		Arg	Glu		
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10	TAC	ACC	ATT	AGT	AGC	CAA	CTA	GAT	ŢTC	AAT	ACG	ACT	CGC	AAC	CAC	ACC	578	5
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15	Ile	Lys	Cys	Leu	Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	626	•
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20				130				p	135	210	Zp.	ser	ьys	140	Thr	Leu		
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	GTG	CTC	TTT	GGG	GCA	GGA	TTC	GGC	GCA	GTA	ATA\	ACA	GTC	GTC	GTC	ATC	722	
	vai	Leu	145	GIY	Ala	GIY	Pne	150	Ala	Val	Ile	Thr		Val	Val	Ile		
25								130					155					
	GTT	GTC	ATC	ATC	AAA	TGC	TTC	TGT	AAG	CAC	GGT	CTC	ATC	TAC	CAT	TTG	770	
h.	Val	Val 160	Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Gly	Leu	<b>\</b> Ile	Tyr	His	Leu		
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30	CAA	CTG	ACC	TCT	TCT	GCA	AAG	GAC	TTC	AGA	AAC	СТА	GCA	Стъ́.	CCC	ጥሮር	818	
	Gin .	Leu	Thr	Ser	Ser	Ala	Lys	Asp	Phe	Arg	Asn	Leu	Ala	Leu	Pro	Trp	010	
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	CTC	TGC .	AAA	CAC	GGT	тст	СТЪ	CCT	C	GCC	TOT	CCA	CTC					
35	Leu (	Cys	Lys :	His	Gly	Ser	Leu	Gly	Glu	Ala	Ser	Ala	Val	TIA	TGC . Cve	AGA Ara	866	
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	AGT :	Thr (	Gln '	ACG Thr	Asn	GAA Glu	CCA Pro	CAG Gln	TAGI	TCTG	CT G	TTTC	TGAG	G AC	GŤAG'	TTTA	920	
40				210											_ \			
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	GAGA	CTGA	AT TO	CTTT	GGAA	A GG	ACAT.	AGGG	ACA	GTTT.	GCA	CATT	TGCT	TG C	ACAT	CACAC	980	
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	TCTCT	rctc:	rc to	CTCT	CTCT	C GA'	TACC'	TTAG	GAT	AGGG	TTC '	TACC	CTGT	TG C	rcag:	rgaca	1100	
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	AAGA	41 CA	JT C.	rGTG	GCGG	A GG	CAGG	CTTC	AAG	CTTG	CAG	CAAT	CCTC	CT G	CACC	AGTTT\	1160	
50	CCTG	AGTG	CC AC	GACT	TCCA	G GT	GTAA	GCTA	TGG	CACT'	TAG (	CAGA	מרארי	דא כי	י אייטייי	ATCAA \	1220	
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•	TGAAG	SAÇA	CT G	AGGT	TCCA	A GA	GGA/	ACCT	GAA	TTAT	GAA (	GGTG	AGTC	AG AZ	ATCC	AGATT	1280	
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55																	1340	
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	(2	) IN	FORM	ATIO	N FO	R SE	Q ID	No:	11:					-		
10			(i)	(. (:	A) Li B) T	E CHI ENGTI YPE: OPOLO	H: 2	14 a	mino cid		ds					
			(ii)	MOL	ECULI	E TYI	PE: 1	prote	ein\							
15			(xi)	SEQ	JENCI	E DES	SCRII	PTIO	1: S	ΕΌ 11	ои с	11:				
	Met	t Ala	a Cys	s Ası	n Cys	Glr	ı Leı	ı Met	Glı	n Ası		Pro	Let	ı Leı	1 Ly:	s Phe 5
20	Pro	o Cys	s Pro	20	g Leu )	ılle	e Lev	Lev	Phe 25	e Val	Leu	ı Leı	ı Ile	Arg		ı Ser
25	Glr	ı Val	Ser 35	Ser	Ala	Asp	Phe	Ser 40	Thr	Pro	Asp	Ile	Thr 45		ı Sei	Gly
Juby	Asn	Pro 50	Ser	Ala	Asp	Thr	Lys 55	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly .
30	Phe 65	Pro	Lys	Pro	Arg	Phe 70	Ser	Trp	Leu	Glu	Asn 75	Gly	Arg	Glu	Leu	Pro 80
	Gly	Ile	Asn	Thr	Thr 85	Ile	Ser	Gln	Asp	Pro 90		Ser	Glu	Leu	Tyr 95	Thr
35	Ile	Ser	Ser	Gln 100	Leu	Asp	Phe	Asn	Thr 105	Thr	Arg	Asn	His	Thr	Ile	Lys
40	Cys	Leu	Ile 115	Lys	Tyr	Gly	Asp	Ala 120	His	Val	Ser	Glu	Asp 125	Phe	Thr	Trp
	Glu	Lys 130	Pro	Pro	Glu	Asp	Pro 135	Pro	Asp	Ser	Lys	Asn 140	Thr	Leu	Val	Leu
45	Phe 145	Gly	Ala	Gly	Phe	Gly 150	Ala	Val	Ile	Thr	Val 155	Val	Val	Ile	Val	Val 160
50					165					170	Ile				175	\
50	Thr	Ser	Ser	Ala 180	Lys	Asp	Phe	Arg	Asn 185	Leu	Ala	Leu -	Pro	Trp 190	Leu	Cys
	Lys	His	Gly 195	Ser	Leu	Gly	Glu	Ala 200	Ser	Åla	Val	Ile	Cys	Arg	Ser	Thr

Gln Thr Asn Glu Pro Gln 

(2) INFORMATION FOR SEQ ID NO:12:

5	•	<b>:</b>	1	EQUEN (A) I (B) 7 (C) S (D) 7	LENGT TYPE : STRAN	TH: I nuc IDEDN	l261 cleic NESS	base ac: do:	e pa: id	irs					·			
		(ii	) MC	DLECU	LE I	YPE:	cDN	IA\									٠	
10		(ix	. (	EATUR (A) N	IAME/				135				•					
15		(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	N DI	10:12						-	
	AGN	CCCN	AGA	TTAT	TTCT	cc c	TGTA	DAAT.	G GA	rceco	CAGG	AGG	CCTG	GGG	AGCG	GACA	\G	60
20	GCT	CCTT	TTA	CTTT	TCTT	CT T	CTTC	TATT	T TI	TTTA	CCTI	CTA	TTTT	ТТТ	CTTC	ATGTT	C.	120
												\				GTGGĄ	rG	180
25 \(\cdot\).	AGG	CACT	GGT	GAC :	ATG Met 1	TAT Tyr	GTC Val	ATC Ile	AAG Lys 5	ACA Thr	TGT Cys	GCA Ala	ACC Thr	TGC Cys 10	ACC . Thr 1	ATG Met		229
30	GGC Gly	TTG	GCA Ala 15	ATC	CTT Leu	ATC Ile	TTT Phe	GTG Val 20	Thr	GTC Val	TTG Leu	CTG Leu	ATC Ile	TCA Ser	GAT Asp	GCT Ala		277
- -	GTT Val	TCC Ser 30	GTG Val	GAG Glu	ACG Thr	CAA Gln	GCT Ala 35	TAT Tyr	TTC Phe	AAT Asn	GGG Gly	ACT Thr	GCA Ala	TAT Tyr	CTG Leu	CCG Pro		325
35	TGC Cys 45	CCA Pro	TTT Phe	ACA Thr	AAG Lys	GCT Ala 50	CAA Gln	AAC Asn	ATA Ile	AGC Ser	CTG Leu 55	AGT Ser	GAG Glu	CTG Leu	GTA Val	GTA Val		373
40	TTT Phe	TGG Trp	CAG Gln	GAC Asp	CAG Gln 65	CAA Gln	AAG Lys	TTG Leu	GTT Val	CTG Leu 70	TAC Tyr	GAG Glu	CAC His	TAT Tyr	TTG Leu 75	GGC Gly		421
45	ACA Thr	GAG Glu	AAA Lys	CTT Leu 80	GAT Asp	AGT Ser	GTG Val	AAT Asn	GCC Ala 85	AAG Lys	TAC Tyr	CTG Leu	GGC Gly	CGC Arg 90	ACG Thr	AGC Ser		469
50	TTT Phe	GAC Asp	AGG Arg 95	AAC Asn	AAC Asn	TGG Trp	ACT Thr	CTA Leu 100	CGA Arg	CTT	CAC	AAT Asn	GTT Val 105	CAG Gln	ATC Ile	AAG Lys	`	517
55	GAC Asp	ATG Met 110	GGC Gly	TCG. Ser	TAT Tyr	GAT Asp	TGT Cys 115	TTT Phe	ATA Ile	CÄA Gln	AAA Lys	AAG Lys 120	CCA Pro	CCC Pro	ACA Thr	GGA Gly		565
•	TCA Ser 125	ATT Ile	ATC Ile	CTC Leu	CAA Gln	CAG Gln 130	ACA Thr	TTA Leu	ACA Thr	GAA Glu	CTG Leu 135	TCA Ser	GTG Val	ATC Ile	GCC Ala	AAC Asn 140		613

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	TTC Phe	AGT Ser	GAA	CCT Pro	GAA Glu 145	Ile	AAA Lys	CTG	GCT Ala	CAG Gln 150	Asr	GTA Val	ACA Thr	A GGA	AAT Asn 155	TCT Ser		661
5	GGC Gly	ATA Ile	AAT Asn	TTG Leu 160	Thr	TGC Cys	ACG Thr	TCT Ser	AAG Lys 165	Gln	GGI Gly	CAC His	CCG	AAA Lys 170	Pro	AAG Lys		709
10	AAG Lys	ATG Met	TAT Tyr 175	TTT Phe	CTG Leu	ATA Ile	ACT Thr	AAT Asn 180	TCA Ser	ACT Thr	AAT Asn	GAG Glu	TAT Tyr 185	Gly	GAT Asp	AAC Asn	·	757
15	ATG Met	CAG Gln 190	ATA Ile	TCA Ser	CAA Gln	GAT Asp	AAT Asn 195	GTC Val	ACA Thr	GAA Glu	CTG Leu	TTC Phe	AGT Ser	ATC Ile	TCC Ser	AAC Asn		805
20	AGC Ser 205	CTC Leu	TCT Ser	CTT Leu	TCA Ser	TTC Phe 210	CCG Pro	GAT Asp	GGT Gly	GTG Val	TGG Trp 215	Hìs	ATG Met	ACC Thr	GTT Val	GTG Val 220		853
	TGT Cys	GTT Val	CTG Leu	GAA Glu	ACG Thr 225	GAG Glu	TCA Ser	ATG Met	AAG Lys	ATT Ile 230	TCC Ser	TCC Ser	AAA Lys	CCT Pro	CTC Leu 235	AAT Asn		901
25 J	TTC	ACT Thr	CAA Gln	GAG Glu 240	TTT Phe	CCA Pro	TCT Ser	CCT Pro	CAA Gln 245	ACG Thr	TAT Tyr	TGG Trp	AAG Lys	GAG Glu 250	ATT Ile	ACA Thr		949
30	GCT Ala	TCA Ser	GTT Val 255	ACT Thr	GTG Val	GCC Ala	CTC Leu	CTC Leu 260	CTT Leu	GTG Val	ATG Met	CTG Leu	CTC Leu 265	ATC Ile	ATT Ile	GTA Val		997
35	TGT Cys	CAC His 270	AAG Lys	ÀAG Lys	CCG Pro	AAT Asn	CÁG Gln 275	CCT Pro	AGC Ser	AGG Arg	CCC Pro	AGC Ser 280	AAC Asn	ACA Thr	GCC Ala	TCT Ser		1045
40	AAG Lys 285	TTA Leu	GAG Glu	CGG Arg	GAT Asp	AGT Ser 290	AAC Asn	GCT Ala	GAC Asp	AGA Arg	GAG Glu 295	ACT Thr	ATC Ile	AAC Asn	CTG Leu	AAG Lys 300	:	1093
	GAA Glu	CTT Leu	GAA Glu	CCC Pro	CAA Gln	ATT Ile	GCT Ala	TCA Ser	GCA Ala	AAA Lys	CCA Pro	AAT Asn	GCA Ala	GAG Glu			}	135

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1195

AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA

1255

AAGAAC

1261

# (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Met Tyr Val Ile Lys Thr Cxs Ala Thr Cys Thr Met Gly Leu Ala Ile 5 5 10 : 5 Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu 25 Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr 10 Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp 50 55 15 Gln Gln Lys Leu Val Leu Tyr Glu His\Tyr Leu Gly Thr Glu Lys Leu 75 Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn 20 Asn Trp Thr Leu Arg Leu His Asn Val Gln le Lys Asp Met Gly Ser 110 25 Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu 120 Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro 130 135 140 30 Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu 150 155 Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe 35 Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser 185 190 Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn Ser Leu\Ser Leu 40 200 Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val Cys Val Leu Glu 45 Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu 230 Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr 50 245 250 Val Ala Leu Leu Val Met Leu Leu Ile Ile Val Cys His Lys Lys 260 265 55 Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg

Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro

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Gln Il	e Ala Ser A	la Lvs	\ Pro Asn :	Ala Glu
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(2) IN	FORMATION FO	OR SEQ	ID NO:14	:
(:	) SEQUENCE	CHARAC	TERISTIC	S:
			3 base\pa	
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	(D) TOPO			
(ii	.) . MOLECULE	TYPE:	cDNA	
(ix	) FEATURE:			\
	(A) NAME	/KEY: (	CDS	\
			194223	\

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGGCCTGGGG AGCGGACAAG 60 120 CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGT CCCTGAGCGC CGAGGTGGAG 180 AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC 223 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys

35

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

40

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
- 45 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
  - (2) INFORMATION FOR SEQ ID NO:16:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1716 base pairs
  - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

OBYCHES LOPY

(A) NAME/KEY: CDS (B) LOCATION: 249..1166

5	(xi)	SEQUENCE	DESC	RIPTION:	SEQ	ID	NO:16:
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5		(xi	i) SI	EQUEN	ICE I	ESCR	IPTI	ON:	SEQ	ID N	10:16	5:						
•	GAG	TTT	ATA	CCTC	AATA	GA C	тетт	ACTA	G TI	TCTC	TTT	TC#	AGGT"	rgtg	AAA	CTCAA	cc .	60
10	TTC	'AAAC	ACA	CTCT	GTTC	CA T	ттст	GTGG	A CI	ATAA	GGAI	CAI	CTT	ragc	ATCI	rgccg	GG	120
•	TGG	ATGO	CAT	CCAG	GCTT	'CT T	TTTC	TACA	T CT	CTGI	TTCI	CGA	\TTT1	TGT	GAGO	CTAG	GA	180
	GGT	GCCI	AAG	CTCC	ATTG	GC T	CTAG	АТТС	Ç TG	GCTI	TCCC	CAI	CATO	TTC	TCCA	AAGC	AT	240
15	CTG	AAGC	T AT Me	G GC t Al	T TG a Cy	C AA s As	n Cy	T CA s Gl 5	G TT n Le	G AT u Me	G CA t Gl	n As	T AC	A CO	A CI	C CTO	2	290
20	AAG Lys 15	Phe	CCA Pro	TGT Cys	CCA Pro	AGG Arg 20	CTC Leu	AAT Asn	CTT Leu	CTC	TTT Phe 25	Val	CTG Leu	CTG Leu	ATT Ile	CGT Arg		338
25	CTT Leu	TCA Ser	CAA Gln	GTG Val	TCT Ser 35	TCA Ser	GAT Asp	GTT Val	GAT Asp	GAA Glu 40	CAA Gln	CTG	TCC Ser	AAG Lys	TCA Ser 45	GTG Val		386
30	AAA Lys	GAT Asp	AAG Lys	GTA Val 50	TTG Leu	CTG Leu	CCT Pro	TGC Cys	CGT Arg 55	TAC Tyr	AAC Asn	TCT Ser	CCT	CAT His	GAA Glu	GAT Asp		434
bol.	GAG Glu	TCT Ser	GAA Glu 65	Asp	CGA Arg	ATC Ile	TAC Tyr	TGG Trp 70	CAA Gln	AAA Lys	CAT His	GAC Asp	AAA Lys 75	\Val	GTG Val	CTG Leu		482
35	TCT Ser	GTC Val 80	ATT Ile	GCT Ala	GGG Gly	AAA Lys	CTA Leu 85	AAA Lys	GTG Val	TGG Trp	CCC Pro	GAG Glu 90	TAT Tyr	AAG Lys	AAC Asn	CGG Arg		530
40	ACT Thr 95	TTA Leu	TAT Tyr	GAC Asp	AAC Asn	ACT Thr 100	ACC Thr	TAC Tyr	TCT Ser	CTT Leu	ATC Ile 105	ATC Ile	CTG Leu	GGC Gly	CTG Leu	GTC Val		578
45	CTT Leu	TCA Ser	GAC Asp	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	GTC Val 120	GTT Val	CAA Gln	AAG Lys	AAG Lys	GAA Glu 125	AGA Arg		626
5.0	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG .Leu	GCT Ala 135	TTA Leu	GTA Val	AAG Lys	TTG Leu	TCC Ser 140	ATC Ile	AAA Lys		674
	GCT Ala	GAC Asp	TTC Phe 145	TCT Ser	ACC Thr	CCC Pro	AAC Asn	ATA Ile 150	ACT Thr	GAG Glu	TCT Ser	GGA Gly	AAC Asn 155	CCA Pro	TCT Ser	GCA Ala		722
55	GAC Asp	ACT Thr 160	AAA Lys	AGG Arg	ATT Ile	ACC Thr	TGC Cys 165	TTT Phe	GCT Ala	TCC Ser	GGG Gly	GGT Gly 170	TTC Phe	CCA Pro	AAG Lys	CCT Pro	-	370

				300	- 65 -			
	CGC TTC Arg Phe 175	TCT TGG TT Ser Trp Le	G GAA AAT u Glu Asn 180	GGA AGA Gly Arg	GAA TTA Glu Leu 185	Pro Gly	ATC AAT ACG Ile Asn Thr 190	818
5	ACA ATT Thr Ile	TCC CAG GA Ser Gln As	p Pro Glu	TCT GAA Ser Glu	TTG TAC Leu Tyr 200	ACC ATT	AGT AGC CAA Ser Ser Gln 205	866
10	CTA GAT Leu Asp	TTC AAT AC Phe Asn Th 210	G ACT CGC r Thr Arg	AAC CAC Ash His	ACC ATT	Lys Cys	CTC ATT AAA Leu Ile Lys 220	914
15	Tyr Gly	GAT GCT CA Asp Ala Hi 225	GTG TCA Val Ser	GAG GAC Glu Asp 230	TTC ACC	TGG GAA 7 Trp Glu 3 235	AAA CCC CCA Lys Pro Pro	962
20	GAA GAC Glu Asp 240	CCT CCT GA Pro Pro As <sub>l</sub>	AGC AAG Ser Lys 245	AAC ACA Asn Thr	CTT GTG Leu Val	CTC TTT ( Leu Phe ( 250	GGG GCA GGA Gly Ala Gly	1010
20	TTC GGC (Phe Gly 2	GCA GTA ATA Ala Val Ile	ACA GTC Thr Val 260	GTC GTC Val Val	ATC GTT Ile Val 265	GTC ATC A	ATC AAA TGC Ile Lys Cys 270	1058
25	TTC TGT I	AAG CAC AGA Lys His Arg 275	Ser Cys	TTC AGA Phe Arg	AGA AAT Arg Asn 280	GAG GCA A	AGC AGA GAA Ser Arg Glu 285	1106
30	ACA AAC A	AAC AGC CTT Asn Ser Leu 290	ACC TTC	GGG CCT Gly Pro 295	GAA GAA Glu Glu	Ala Leu A	GCT GAA CAG la Glu Gln	1154
35	Thr Val I	FTC ĊTT TAG Phe Leu 305	TTCTTCT C	TGTCCATG	T GGGATA	CATG GTAT	TATGTG	1206
	GCTCATGAG	G TACAATCI	TT CTTTCA	GCAC CGT	GCTAGCT	GATCTTTCG	G AÇAACTTGAC	1266
40	ACAAGATAG	SA GTTAACTG	GG AAGAGA	AAGC CTT	GAATGAG	GATTTCTTT	C CATCAGGAAG	1326
.0	CTACGGGCA	AA GTTTGCTG	GG CCTTTG	ATTG CTT	GATGACT	GAAGTGGAA	A GGCTGAGCCC	1386
	ACTGTGGGT	G GTGCTAGC	CC TGGGCA	GGGG CAG	GTGACCC	TGGGTGGTA	T AAGAAAAAGA	1446
45	GCTGTCACT	TA AAAGGAGA	GG TGCCTA	GTCT TAC	TGCAACT	TGATATGTC	A TGTTTGGTYTG	1506
	GTGTCTGTG	G GAGGCCTG	CC CTTTTC	rgaa gag	AAGTGGT (	GGGAGAGTG	G ATGGGGTGGG	1566
50	GGCAGAGGA	A AAGTGGGG	GA GAGGGC	CTGG GAG	GAGAGGA (	GGGAGGGG.	A CGGGGTGGGG	1626
			•	•	ATAATAA 1	TATAAATAT	T AAATAAAAG \	1686
55	AGAGTATTG	A GCAAAAA	KAAAAA AA	AAAA			•	1716
	(0)							*

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 306 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe

1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
35 40 45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser 50 55 60

20 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val 65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
85 90 95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser \Ile Lys Ala Asp

35 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr 145 150 155 160

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
165 170 175

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
180 185 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
45 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly 210 215 220

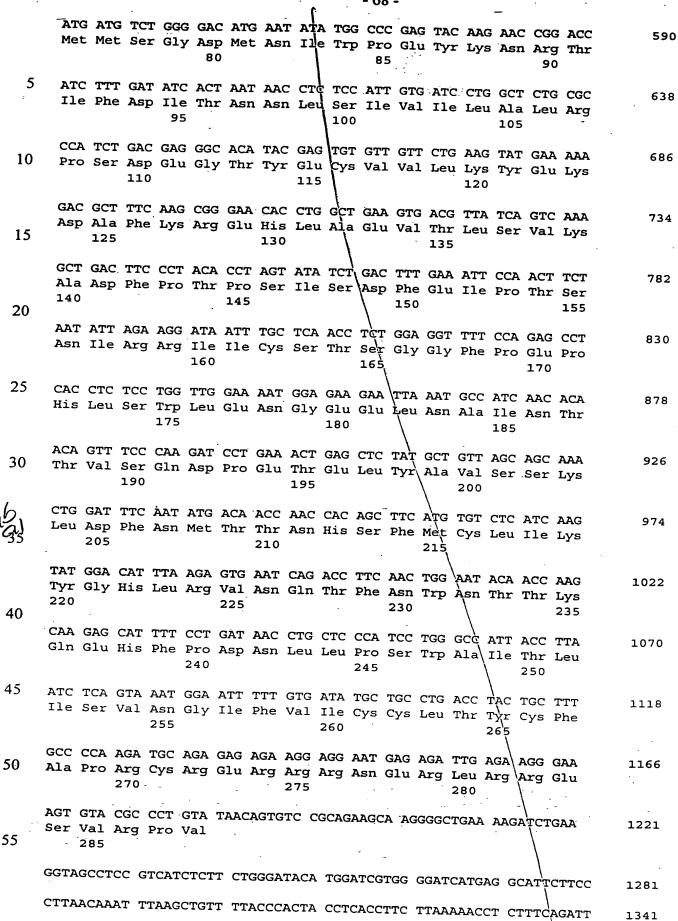
Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp 225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly 245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys 260 265 270



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	Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn 275 280 285	ŧ
5	Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val 290 295 300	
	Phe Leu 305	
10	(2) INFORMATION FOR SEQ ID NO:18:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 1491 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: CDNA	
20	(ix) FEATURE: (A) NAME/KEY: CDS	
25	(B) LOCATION: 3181181	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
•	CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT	60
30	GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTTCT TCAGCAAGCT	120
24	GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT	180
35	GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT	240
	TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC	300
40	CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA  Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro  1 5 10	350
45	TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly 15 20 25	398
73	CTT TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys	446
50	GAA GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu 45 50 55	494
55	GCA CAA ACT CGC ATC TAC TGG CAA AAG GAG AAA ATG GTG CTG ACT Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr 65 70 75	542



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AAG	CTG	AACA	GTT	ACAAG	TAE	GCT	GCA1	C C	CTCTC	CTT	CTC	CCC	ATAT	GCA	ATTTO	CT
TAA	TGT	AACC	TCT	CTTI	TTG d	CATO	TTTC	CA	TCTC	CCAI	CT	rgaa:	rtgt	CTT	STCAC	CC
AAT	TCAT	TAT	CTAT	PTAÁA 	CA C	TAAT	TTGA	uG .							-	
(2)	INE	ORM	TION	FOR	SEÇ	D ID	WO:1	9:								
		(i)	( <i>P</i>	JENCE (A) LE (B) TY (D) TO	NGTH PE:	: 28 amin	8 am	ino įd		s						
	(	ii)	MOLE	CULE	TYP	E: p	rote	in \	\							
	(	xi)	SEQU	ENCE	DES	CRIP	TION	: SE		NO:	19:					
Met 1	Gly	His	Thr	Arg 5	Arg	Gln	Gly	Thr	Ser 10	Pro	Ser	Lys	Cys	Pro	_	
Leu	Asn	Phe	Phe 20	Gln	Leu	Leu	Val	Leu 25		gly	Leu	Ser	His 30		Cys	
Ser	Gly	Val 35	Ile	His	Val	Thr	Lys 40	Glu	Val	Lys	\Glu	Val 45		Thr	Leu	
Ser	Cys 50	Gly	His	Asn	Val	Ser 55	Val	Glu	Glu	Leu	Ala 60	Gln	Thr	Arg	Ile	
Tyr 65	Trp	Gln	Lys ·	Glu	Lys 70	Lys	Met	Val	Leu	Thr 75	Met	Met	Ser	Gly	Asp 80	
Met	Asn	Ile	Trp	Pro 85	Glu	Tyr	Lys	Asn	Arg 90	Thr	Ile	Phe	Asp	Ile 95	Thr	
Asn	Asn	Leu	Ser 100	Ile	Val	Ile	Leu	Ala 105	Leu	Arg	Pro	Ser	Asp 110	Glu \	Gly	
Thr	Tyr	Glu 115	Cys	Val	Val	Leu	Lys 120	Tyr	Glu	Lys	Asp	Ala 125		Lys	Arg	
Glu	His 130	Leu	Ala	Glu	Val	Thr 135	Leu	Ser	Val	Lys	Ala 140	Asp	Phe	Pro	Thr	
Pro 145	Ser	Ile	Ser	Asp	Phe 150	Glu	Ile	Pro	Thr	Ser 155	Asn	Ile	Arg	Arg	Ile 160	
Ile	Cys	Ser	Thr	Ser 165	Gly	Gly	Phe	Pro	Glu 170	Pro	His	Leu	Ser	Trp 175	Leu	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
Glu	Asn	Gly	Glu 180	Glu	Leu	Asn		Ile 185	Asn	Thr	Thr	Val	Ser 190	Gln	Asp	
Pro	Glu	Thr 195	Glu	Leu	Tyr	Ala 	Val 200	Ser	Ser	Lys	Leu	Asp 205	Phe	Asn	Met	\

	Thi	210	Asr	His	s Se:	r Phe	21!	<b>Cy</b>	s Le	u Ile	E Lys	220		y Hi	s Leu	Arg	٠
5	Val 225	Asn 5	Gln	Thr	Phe	230	Tri	) Ası	n Th	r Thr	Lys 235		ı Glı	u Hi	s Phe	Pro 240	
	Asp	Asn	Leu	Leu	245	Ser	TI	Ala	a Ile	250	Leu	Ile	Se:	r Va	l Asn 255		
10	Ile	Phe	Val	11e 260	Суя	cys	Leu	Thi	Ty:	Cys	Phe	Ala	Pro	27	g Cys	Arg	
15	Glu	Arg	Arg 275	Arg	Asr	Glu	Arg	280	à Arg	Arg	Glu	Ser	Val 285		J Pro	Val	
	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 2	20:	\						,	
20		(i)	() ()	A) L: B) T C) S'	ENGT YPE : TRAN	HARA H: 1 nuc DEDN OGY:	151 leic ESS:	base aci dou	pai d	rs	\						
25		(ii)	MOI	LECU	LE T	YPE:	CDN	A			\.				٠		
Sola Sola	1	(ix)		A) N2	AME/	KEY: ION:		.102	5						,		
-		(xi)	SEÇ	ÜENC	CE D	ESCR:	IPTI	ON:	SEQ :	ID NO	):20:	\	\				
35	GGAG	GCAAG	CA G	SACGO	GTA	AG AG	GTGG(	CTCC'	T GT	AGGCZ	AGCA	CGGZ	CŢŢ	GAA	CAACC	AGACT	. 60
	CCT	TAGA	CG I	GTTC	CAG	AA CI	TAC	GAA(	G CA	CCAC					GA TG		111
40												1			_	5	
	ACC Thr	ATG Met	GGC Gly	TTG Leu	GCA Ala 10	ATC Ile	CTT Leu	ATC Ile	TTT Phe	GTG Val 15	ACA Thr	GTC Val	TTG Leu	CTG, Leu	ATC lle \20	TCA Ser	161
45	GAT Asp	GCT Ala	GTT Val	TCC Ser 25	GTG Val	GAG Glu	ACG Thr	CAA Gln	GCT Ala 30	TAT Tyr	TTC . Phe .	AAT Asn	GGG Gly	ACT Thr 35	GCA '	TAT Tyr	209
	CTG	CCG	тсс	CCN	daran.	ACA	AAG	GCT	CAA	AAC .	ATA .	AGC	CTG	AGT	GAG (	) CTG	257
50	Leu	Pro	Cys 40	Pro	Phe	Thr	Lys	Ala 45	Gln	Asn	Ile :	Ser	Leu 50	Ser	Glu i	Leu	
50 55	GTA	Pro   GTA	Cys 40 TTT	Pro TGG	Phe CAG	Thr	Lys CAG	Ala 45 CAA	Gln AAG	Asn TTG	Ile :	Ser CTG	Leu 50	Ser	CAC THIS	Lèu	305



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	ACG	AGC	TTT	GAC	AGG	ÀAC	AAC	TGG	ACT	CTA	CGA	CTI	CAC	: AAT	GTI	CAG	401	
	Thr	Ser	Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg	Leu	His	Asn	Val	Gln	401	
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	ATC	AAG	GAC	ATG	GGC	TCG	TĄT	GAT	TGT	TTT	ATA	CAA	AAA	AAG	CCA	CCC	449	ļ
	Ile	Lys	Asp	Met	Gly	Ser	Tylp	Asp	Cys	Phe	Ile	Gln	Lys	Lys	Pro	Pró		
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10	ACA	GGA	TCA	ATT	ATC	CTC	CAA	ÇAG	ACA	TTA	ACA	GAA	CTG	TCA	GTG	ATC	497	
	1111	Gly	120	TTE	TTE	ьeu	GIN		Thr	Leu	Thr	Glu			Val	Ile		
			120					125					130					
	GCC	AAC	TTC	AGT	GAD	- רכיתי	GAA	מיד מ	מממ	CTC	COT	CNC	3 3 m	- Cm				
15	Ala	Asn	Phe	Ser	Glu	Pro	Glu	Tle	T.vs	Len	Ala	Gla	AAT	GTA	ACA	GGA	545	
		135					140		733	Deu	ALG	145	ASII	vai	inr	GIY	•	
												113						
	AAT	TCT	GGC	ATA	AAT	TTG	ACC	TGC	ACG	TCT	AAG	CAA	GGT	CAC	CCG	מממ	593	
	Asn	Ser	Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys	Gln	Glv	His	Pro	Lvs	373	
20	.150					155			\		160					165		
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	CCT	AAG	AAG	ATG	TAT	TTT	CTG	ATA	ACT	TAA	TCA	ACT	AAT	GAG	TAT	GGT	641	
	Pro	Lys	Lys	Met	Tyr	Phe	Leu	Ile	Thr	A\sn	Ser	Thr	Asn	Glu	Tyr	Gly	•	
25					170					17/5					180			
23	CAM	220	3 ma	a. a						_ \								
	ACD	AAC	Mot	CAG	ATA	TCA	CAA	GAT	AAT	GTC	ACA	GAA	CTG	TTC	AGT	ATC	689	
	ASP	Asn	Met	185	TIE	ser	GIN	Asp.		Val	Thr	Glu	Leu		Ser	Ile		
				105					190		\			195				
30	TCC	AAC	AGC	СТС	ידי	СТТ	тсъ	ጥጥር	CCG	CAT		CTC	maa.	~~ m	3.55			
	Ser	Asn	Ser	Leu	Ser	Leu	Ser	Phe	Pro	Asn	GIV	ובעו) בעו	TGG	CAT	Mot	ACC	737	
			200					205		nsp	GIY	Vai	210	nis	Met	Thr		
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	GTT	GTG	TGT	GTT	CTG	GAA	ACG	GAG	TCA	ATG	AAG	ATT	TCC	TCC	ααα	ССТ	785	
35	Val	Val	Cys	Val	Leu	Glu	Thr	Glu	Ser	Met	Lys	Ile	Ser	Ser	Lvs	Pro	, , , , ,	
Ь		215		•			220				_	225	\		-2			
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<i>O</i> .	CTC	TAA	TTC	ACT	CAA	GAG	TTT	CCA	TCT	CCT	CAA	ACG	TAT	TGG	AAG	GAG	833	
40	230	Asn	Phe	Thr	Gln	Glu	Phe	Pro	Ser	Pro	Gln	Thr	Туд	$\mathtt{Trp}$	Lys	Glu		-
70	230					235					240		\			245		
	ATT	ACA	CCT	TCA	CTT	λСπ	CTC	ccc	CMC	ama	omm.	~~~		<b>\</b>				
	Ile	ACA Thr	Ala	Ser	Val	Thr	Usl Usl	73 a	LOU	CTC	CTT	GTG	ATG	CTG	CTC	ATC	881	
			•••	<b></b>	250		vaı	AIA	Leu	255	Leu	vai	met	ьęи		Ile		
45										233				- /	260			
	ATT	GTA	TGT	CAC	AAG	AAG	CCG	AAT	CAG	ССТ	AGC	AGG	CCC	vcc/	מ מ מ	202	000	
	Ile	Val	Cys	His	Lys	Lys	Pro	Asn	Gln	Pro	Ser	Ara	Pro	Ser	) Aen	Thr	929	
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50	GCC	TCT .	AAG	TTA	GAG	CGG	GAT	AGT	AAC	GCT	GAC	AGA	GAG	ACT	) DTA	AAC	977	•
-	Ala	Ser	Lys	Leu	Glu	Arg -	Asp -	Ser	Asn	Ala	Asp	Arg	Glu	Thr	īle	Àsn		
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	7	CIONIIGGA AII	CIACAGI	IGAATAATTA	1145
AAGAAC					1151
	1				
(2) INFORMATION FOR	R SEQ ID NO:21:			_	
(i) SEQUENCE	E CHARACTERISTICS	S:		-	
	ENGTH: 309 amino				
	YPE: amino acid	\	•		
(D) ŢĊ	OPOLOGY: linear	1			
(ii) MOLECULE	TYPE: protein				
(xi) SEQUENCE	E DESCRIPTION: SE	Q ID NO:21:		÷	
W-4-2-		\			
Met Asp Pro Arg Cys		<b>\</b>	Ile Phe	Val Thr	
1 5	•	10		15	
Val Leu Leu Ile Ser	Asp Ala Val Ser	Val Glu Thr	Gln Ala	Tur Dhe	
20	25		30	<del>-</del>	

50 5'5 Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala 30

Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr tys Ala Gln Asn Ile

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Lys Leu Val

Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Tro Thr Leu Arg

Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile 100 **1/1**0

Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr 120

Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala 130 135

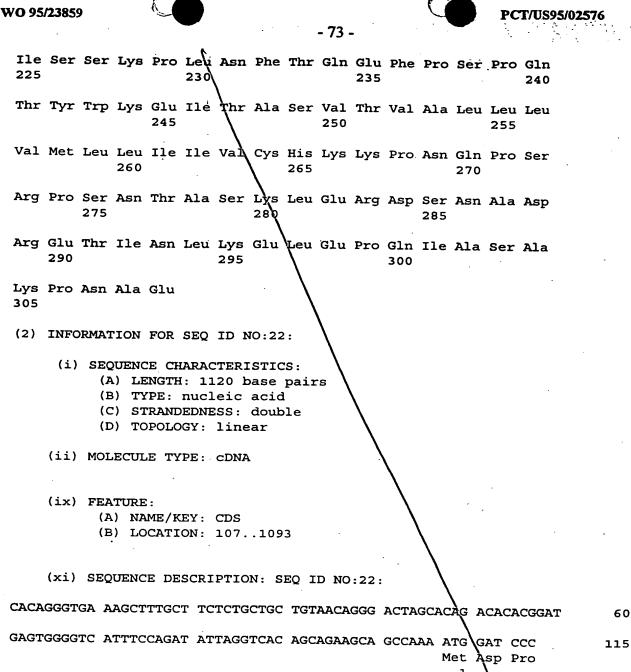
Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys 155 160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn\Ser 170

50 Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr 180 185

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly 195 -\_\_\_\_200

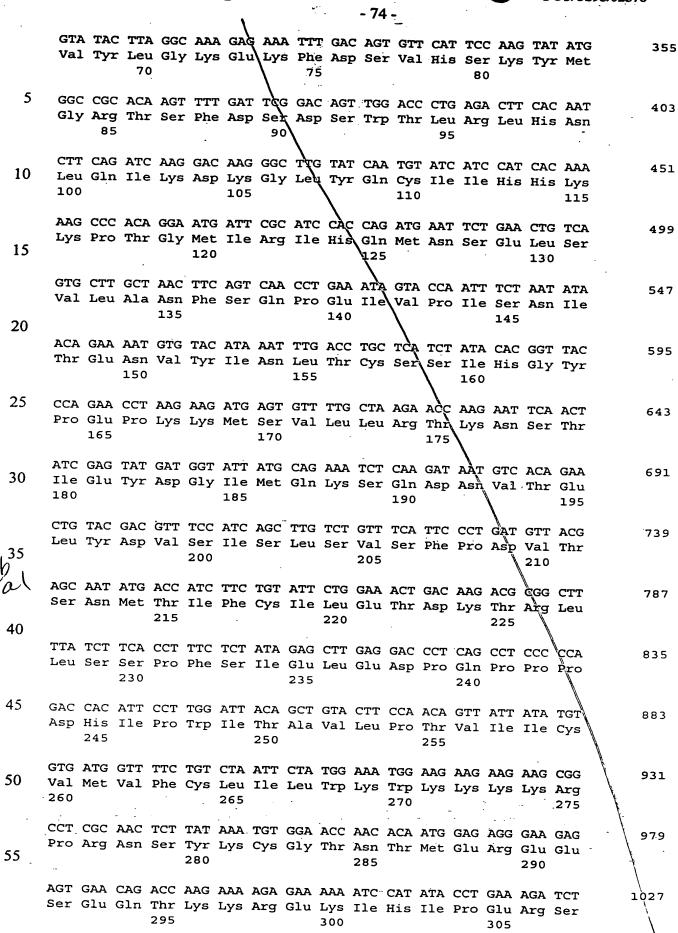
Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys 215



CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu CTC TCT GGT GCT GCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr 

GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser

GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu 





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5	GAT Asp	GAA	GCC Ala 310	CAG Gln	CGT Arg	GTT Val	Phe	AAA Lys 315	AGT	TCG Ser	AÅG Lys	ACA Thr	TCT Ser 320	Ser	TGC Cys	GAC Asp		1075
			Asp	ACA Thr				AATT	AGA	GTAA	AGCC	CA A	AAAA	AA		-		1120
10	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 2	3 /									
•			(i)	SEQU				ERIS' 9 am:			_							
15				(B	) TY	PE:	amin	o ac: line	id \	AC10	ь					-		
		. (	ii)	MOLE	CULE	TYP	E: p	rote	in									
20		(:	xi)	SEQU	ENCE	DES	CRIP'	TION	: SE	Q ID,	NO:	23:						٠
	Met 1	Asp	Pro	Gln	Cys 5	Thr	Met	Gly	Leu	Ser 10	Asn	Ile	Leu	Phe	Val 15	Met		
25	Ala	Phe	Leu	Leu 20	Ser	Gly	Ala	Ala	Pro 25	Leu	Lys/	Ile	Gln	Ala 30	Tyr	Phe		
30	Asn	Glu	Thr 35	Ala	Asp	Leu	Pro	Cys 40	Gln	Phe	Ala	Asn	Ser 45	Gln	Asn	Gln		
50	Ser	Leu 50	Ser	Glu	Leu	Val -	Val 55	Phe	Trp	Gln	Asp	Gl'n	Glu	Asn	Leu	Val		
) 35	Leu 65	Asn	Glu	Val	Tyr	Leu 70	Gly	Lys	Glu	Lys	Phe 75	Asp	Ser	Val	His	Ser 80	-	
•	Lys	Tyr	Met	Gly	Arg 85	Thr	Ser	Phe	Asp	Ser 90	Asp	Ser	Trp,	Thr	Leu 95	Arg		
40	Leu	Hiş	Asn	Leu 100	Gln	Ile	Lys	Asp	Lys 105	Gly	Leu	Tyr	Gln	Cys		Ile		
	His	His	Lys 115	Lys	Pro	Thr	Gly	Met 120	Ile	Arg	Ile	His	Gln 125	Ì	Asn	Ser		
45	Glu	Leu 130	Ser	Val	Leu	Ala	Asn 135	Phe	Ser	Gln	Pro	Glu 140		Val	Pro	Ile		
50	Ser 145	Asn	Ile	Thr	Glu	Asn 150	Val	Tyr	lle	Asn	Leu 155	Thr	Cys	Ser	Ser	Ile 160		
	His	Gly	Tyr	Pro	Glu. 165	Pro	Lys	Lys	Met	Ser. 170	Val	Leu	Leu	Arg	Thr 175			• .
55	Asn	Ser	Thr	Ile 180	-	Tyr	Asp.	Gly	Ile 185		Gln	Lys	Ser	Gln 190		Asn		٠.
	Val	Thr	Glu 195	Leu	Tyr	Asp	Val	Ser 200		Ser	Leu	Ser	Val 205		Phe	Pro		

						- \							_					
	Asp	Val 210	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu 220	Glu	Thr	Asp	Lys	•	
5	Thr 225	Arg	Leu	Leu	Ser	Ser -230	Pro	Phe	Ser	Ile	Glu 235	Leu	Glu	Asp	Pro	Gln 240		-
10	Pro	Pro	Pro	Asp	His 245	Ile	Pro	Trp	Ile	Thr 250	Ala	Val	Leu	Pro	Thr 255	- Val	-	
•	Ile	Ile	Cys	Val 260	Met	Val	Phe	Cys	Leu 265	Ile	Leu	Trp	Lys	Trp 270	Lys	Lys		
15	Lys	Lys	Arg 275	Pro	Arg	Asn	Ser	Tyr\ 280	Lys	Cys	Gly	Thr	Asn 285	Thr	Met	Glu		
	Arg	Glu 290	Glu	Ser	Glu	Gln	Thr 295	Lys	Lys	Arg	Glu	Lys 300	Ile	His	Ile	Pro		
20	Glu 305	Arg	Ser	Asp	Glu	Ala 310	Gln	Årg	Val	Phe	Lys 315	Ser	Ser	Lys	Thr	Ser 320		
25	Ser	Cys	Asp	Lys	Ser 325	Asp	Thr	Cys	Phe		\							
	(2)	INFO	RMAT	'ION	FOR	SEQ	ID N	10:24	:									
30 b		(i)	(A (B (C	) LE ) TY ) ST	E CH NGTH PE: RAND POLO	: 11 nucl EDNE	61 b eic SS:	ase acid doub	pair	s				٠,				
35		(ii)	MOL	ECUL	E TY	PE:	CDNA					. \	\					
40		(ix)		) NAI	: ME/KI CATIO			.1134						\				
		(xi)	SEQ	UENC	E DES	SCRI	PTIO	N: SI	EQ II	NO.	:24:							
15	AGGA	GCCT:	ra go	GAGG:	TACG	G GGZ	AGCT	CGCA	AATA	CTC	CTT 7	TGGT	TTAT	LT C	የጥል ርሳ	CACCT		60
45															\	AGCTA		120
	CAGTO														1			
50			-			-		Met 1	Asp	Pro	Glr	Cys 5	Thr	Met	G1,	` `		171
55	CTG A	GT # Ser # 10	AAC A Asn I	ATT (	CTC I Leu F	TTT C	TG A Val M 15	ATG G	SCC I	TC C	TG C	TC T eu S 20	CT G	GT G	CT C	SCT Lla	-	219
	CCT C Pro L 25	TG A	AG A	ATT C	CAA G	CT I la I 30	AT I	CTC A	AT G sn G	lu T	CT G hr A 35	CA G la A	AC C sp L	TG C	CA T	GC Cys 40		267

						-	-			77			<u> </u>	•			3,023,0	•
				•		1	·	4 (j) (	•	- 77	-							
	CAA Gln	Phe	GCA Ala	AAC Asn	TCT Ser 45	glþ	AAC Asn	CAA Gln	AGC Ser	CTC Lev	ı Ser	GAC	CTA Lev	A GTA	GT# Val	TTT Phe		315
, 5	TGG Trp	CAC Glr	GAC	Gln	Glu	AAC Asn	TTG Leu	GTT Val	Leu	AAT Asn	GAG	GTA Val	TAC	TTA	. GGC	AAA Lys	:	363
10	GAG Glu	AAA Lys	TTT	GAC Asp	AGT	GTT Val	CAT His	TCC Ser	AAG Lys	TAT	ATG	GGC Gly	CGC	70 ACA Thr	AGT	' TTT		411
			75 GAC		•			80					85					450
15	Asp	Ser 90	Asp	Ser	Trp	Thr	Leu 95	Arg	\Leu	His	Asn	Leu 100	Gln	Ile	Lys	Asp		459
20	AAG Lys 105	GGC	TTG Leu	TAT	CAA Gln	TGT Cys 110	ATC Ile	ATC Ile	CAT His	CAC	AAA Lys 115	AAG Lys	CCC Pro	ACA Thr	GGA Gly	ATG Met 120		507
	ATT Ile	CGC Arg	ATC Ile	CAC His	CAG Gln 125	ATG Met	AAT Asn	TCT Ser	GAA Glu	CTG Leu 130	TCA Ser	GTG Val	CTT Leu	GCT Ala	AAC Asn 135	TTC Phe		555
25	AGT Ser	CAA Gln	CCT Pro	GAA Glu 140	ATA Ile	GTA Val	CCA Pro	ATT Ile	TCT Ser 145	AAT Asn	ATA Ile	ACA Thr	GAA Glu	AAT Asn 150	GTG Val	TAC Tyr	,	603
30	ATA Ile	AAT Asn	TTG Leu 155	ACC Thr	TGC Cys	TCA Ser	TCT Ser	ATA Ile 160	CAC His	GGT Gly	TAC Tyr	CCA Pro	GAA Glu 165	CCT Pro	AAG Lys	AAG Lys	(	651
35	ATG Met	AGT Ser 170	GTT	TTG Leu	CTA Leu	AGA Arg	ACC Thr 175	AAG Lys	AAT Asn	TCA Ser	ACT Thr	ATC Ile 180	GAG \Glu	TAT Tyr	GAT Asp	GGT Gly	·-	599
40	ATT Ile 185	ATG Met	CAG Gln	AAA Lys	TCT Ser	CAA Gln 190	GAT Asp	AAT Asn	GTC Val	ACA Thr	GAA Glu 195	CTG Leu	TAC Tyr	GAC Asp	GTT Val	TCC Ser 200	7	747
	ATC Ile	AGC Ser	TTG Leu	Ser	GTT Val 205	TCA Ser	TTC Phe	CCT Pro	GAT Asp	GTT Val 210	ACG Thr	AGC Ser	AAT Asn	ATG Met	ACC Thr 215	ATC Ile	7	795
45	TTC Phe	TGT Cys	ATT Ile	CTG Leu 220	GAA Glu	ACT Thr	GAC Asp	AAG Lys	ACG Thr 225	CGG Arg	CTT Leu	TTA Leu	TCT Ser	TCA Ser 230	CCT Pro	TTC Phe	8	143
50	TCT Ser	ATA Ile	GAG Glu 235-	CTT Leu	GAG Glu	GAC Asp	Pro	CAG Gln 240	CCT Pro	CCC Pro	CCA Pro	Asp	CAC His 245	ATT Ile	CCT Pro	TGG Trp		91
55	тте	ACA Thr 250	GCT Ala	GTA Val	CTT Leu	Pro	ACA Thr 255	GTT Val	ATT Ile	ATA Ile	Cys	GTG Val 260	ATG Met	GTT Val	TTC Phe	TGT Cys	. 9	39
	CTA Leu 265	ATT Ile	CTA Leu	TGG . Trp	Lys	TGG ; Trp ; 270	AAG . Lys	AAG Lys	AAG Lys	Lys	CGG Arg 275	CCT Pro	CGC Arg	AAC Asn	TCT Ser	TAT Tyr 280	9	87



5	AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys 285 290 295	1035
·	AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg 300 305 310	1083
10	GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys 315 320 325	1131
15	TTT TAATTAAAGA GTAAAGCCCA AAAAAAA Phe	1161
20	(2) INFORMATION FOR SEQ ID NO:25:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 629 base pairs  (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: CDNA	•
30	(ix) FEATURE:  (A) NAME/KEY: CDS	
7.h 185. 1	(B) LOCATION: 196  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
	AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA AGA AAG AAG	40
40	Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser  1 5 10 15	48
	CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu 20 25 30	96
45	TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT	156
	CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG	216
50	AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG	276
	CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC ACTGTGGGTG GTGCTAGAAA	336
55	· · · · · · · · · · · · · · · · · · ·	396
<i>55</i>	· ·	456
	1	516
	GAGGGCCTGG GAGGAGAGA GGGAGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG	576

	ga.,	- 79 -	PCT/US95/025	76
A	3003000 s		* · · · · · · · · · · · · · · · · · · ·	

	GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG AGAGTATTGA GCA	62
5	(2) INFORMATION FOR SEQ ID NO:26:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 32 amino acids	
10	(B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
	Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser  1 10 15	
20	Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu 20 25 30	
	(2) INFORMATION FOR SEQ ID NO:27:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 379 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
30 b	(D) TOPOLOGY: linear	
Y'o	(ii) MOLECULE TYPE: cDNA	
35	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 169	•
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
40	TGC TTT GCC CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg 1 5 10 15	48
45	AGG GAA AGT GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA Arg Glu Ser Val Arg Pro Val 20	99
50	AAGATCTGAA GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG	159
- 	GCATTCTTCC CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT	219
<b>5</b>	CTTTCAGATT AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT	27/9
55 -	GCAATTTGCT TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT	339

CTTGTCAGCC AATTCATTAT CTATTAAACA CTAATTTGAG

48

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(2) INFORMATION	FOR	SEO	ID	NO:28
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/ i \	SEQUENCE	CTT 2 D 2 CT	<del></del>
\ <del>_</del> /	SEQUENCE	CHARACT	ERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: Ninear
- (ii) MOLECULE TYPE: protein
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg

1 10 15

- 15 Arg Glu Ser Val Arg Pro Val
  - (2) INFORMATION FOR SEQ ID NO:29:
- 20 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 261 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT AAG
His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys

1 10

40 TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC CTG AAG GAA
Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
20 25

CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG TGAAGGCAGT 145

Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu

GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC 205

50 AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA AAGAAC 261

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii)	MOLECULE	TYPE:	proteir
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# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys 10

Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu 25

Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu 40

### (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 25 (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..183
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAA TGG AAG AAG AAG CGG CCT CGC AAC TCT TAT AAA TGT GGA ACC 48 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr

AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG AAA AGA GAA AAA 96 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys 20

ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT GTT TTT AAA AGT 40 144 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser 40

TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT TTT TAATTAAAGA 45 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe 193 50

## GTAAAGCCCA AAAAAA

210

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein



(xi)	SEQUENCE	DESCRIPTION:	SEO	ID	NO - 32
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Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
1 5 10 15

Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
20 25 30

Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser

35 40 45

Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
50 55 60

# 15 (2) INFORMATION FOR SEQ ID NO:33:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: cDNA

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#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..359

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# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

	GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC	60
35	TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
	TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA	180
40	GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT	240
	CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC  Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  1 5 10	290
45	AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30	338
50	CTT TCA CAA GTG TCT TCA GAT Leu Ser Gln Val Ser Ser Asp 35	359

(2) INFORMATION FOR SEQ ID NO:34:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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<pre>(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:</pre>		
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro	·. :	
Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu 20 25	u Ile Arg Leu Ser	

Pro Cys Pro A 10

Gln Val Ser Ser Asp 35

- 15 (2) INFORMATION FOR SEQ ID NO:35:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 318..416

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

	CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT	60
35	GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTTCT TCAGCAAGCT	120
	GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT	180
40	GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT	240
	TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC	300
45	CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro 1 5 10	350
50	TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly 15 20 25	398
	CTT TCT CAC TTC TGT TCA Leu Ser His Phe Cys Ser 30	416

- (2) INFORMATION FOR SEQ ID NO:36:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 amino acids

	(B) TYPE: amino acid (D) TOPOLOGY: linear
5	(ii) MOLECULE TYPE: protein
J	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
10	Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr 1 5 10 15
10	Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys 20 25 30
15	Ser
	(2) INFORMATION FOR SEQ ID NO:37:
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 113 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
25	(ii) MOLECULE TYPE: cDNA
30	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 99113
2.5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
35	GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60
	CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC 113  Met Asp Pro Arg Cys
40	1 5
	(2) INFORMATION FOR SEQ ID NO:38:
45	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 5 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>
50	(ii) MOLECULE TYPE: protein
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
	Met Asp Pro Arg Cys 1 5
55	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs

(2) INFORMATION FOR SEQ ID NO:39:

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			PC
	_	- 85 -	
(C)	TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear		

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J	(11)	MOLECULE	TYPE	CDMA

(ix) FEATURE:

(A) NAME/KEY: CDS

10 (B) LOCATION: 107..124

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

13	CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
	GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC Met Asp Pro	115
20	1	
	CAG TGC ACT Gln Cys Thr	124

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Asp Pro Gln Cys Thr 1 . 5

- 40 (2) INFORMATION FOR SEQ ID NO:41:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 195 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 148..195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

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TGC	TTCT	etg 1	TCCI	TGG	GA A	_ ATGCT	GCTGT	GCT	TATGC	AT C	TGGT	- CTCT	r TT	IGGAGCTA	120
CAG	TGGAC	CAG G	CATI	TGT	GA C	AGCA	CT AT Me	G GG t Gl	A CTG y Leu	AGT Ser	AAC Asn 5	ATT Ile	CTC Leu	TTT Phe	171
GTG Val	ATG Met 10	GCC Ala	TTC Phe	CTG Leu	CTC Leu	TCT Ser 15	GGT Gly					-		-	195
(2)			EQUE	NCE LEN	CHAI GTH	RACTE	NO:42 ERIST: amino	ICS:	.ds					-	

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## (2) INFORMATION FO

- (i) SEQUENC
  - (A)
  - (B) '
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly 5 10

- (2) INFORMATION FOR SEQ ID NO: 43:
- 30 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
- 40 CCAACATAAC TGAGTCTGGA AA

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
- 55 (2) INFORMATION FOR SEQ ID NO: 45:

CTGGATTCTG ACTCACCTTC A

- - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs

	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:	
10	AGGTTAAGAG TGGTAGAGCC A	21
	(2) INFORMATION FOR SEQ ID NO: 46:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
20	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
25	AATACCATGT ATCCCACATG G	21
25	(2) INFORMATION FOR SEQ ID NO: 47:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
•	(ii) MOLECULE TYPE: oligonucleotide	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:	
	CTGAAGCTAT GGCTTGCAAT T	21
40	(2) INFORMATION FOR SEQ ID NO: 48:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
	TGGCTTCTCT TTCCTTACCT T	21
	(2) INFORMATION FOR SEQ ID NO: 49:	-
55	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 21 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

	· ·	
	(ii) MOLECULE TYPE: oligonucleotide	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
	GCAAATGGTA GATGAGACTG T	. 21
	(2) INFORMATION FOR SEQ ID NO: 50:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic adid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
20	CAACCGAGAA ATCTACCAGT AA	22
	(2) INFORMATION FOR SEQ ID NO: 51:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: \51:	
35	GCCGGTAACA AGTCTCTTCA	20
	(2) INFORMATION FOR SEQ ID NO: 52:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:	
	AAAAGCTCTA TAGCATTCTG TC	22
50	(2) INFORMATION FOR SEQ ID NO: 53:	, <del>.</del>
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	

CTGAGATCAG CAAGACTGTC

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	(xi	SEQUENCE DESCRIPTION: SE	Q ID NO: 53:	:	·
	ACTGACT	TGG ACAGTTGTTC A			
5	(2) INF	ORMATION FOR SEQ TO NO: 54	:	£.	:
10	. (i	SEQUENCE CHARACTERISTICS  (A) LENGTH: 20 base pai  (B) TYPE: nucleic acid  (C) STRANDEDNESS: singl  (D) TOPOLOGY: linear	rs		- -
	(ii)	MOLECULE TYPE: oligonucl	eotide		
15	(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO: 54:		-
	TTTGATGO	AC AACTTTACTA	\		
20	(2) INFO	RMATION FOR SEQ ID NO: 55	: \		
	(i)	SEQUENCE CHARACTERISTICS (A) LENGTH: 20 base pair (B) TYPE: nucleic acid			
25		<pre>(C) STRANDEDNESS: single (D) TOPOLOGY: linear</pre>			
	(ii)	MOLECULE TYPE: oligonucle	eotide \		
30	(xi)	SEQUENCE DESCRIPTION: SEC	Q ID NO: 55:		
	CAGCTCAC	TC AGGCTTATGT	\		
	(2) INFO	RMATION FOR SEQ ID NO: 56	:	tud.	
35 20 40	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pair  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	rs \		
.0	(ii)	MOLECULE TYPE: oligonucle	eotide		
	(xi)	SEQUENCE DESCRIPTION: SEQ	) ID NO: 56:		
45	AAACAGCA	IC TGAGATCAGC A			
	(2) INFO	RMATION FOR SEQ ID NO: 57:		\	
50	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pair  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	`s		<u>.</u>
55	(ii)	MOLECULE TYPE: oligonucle	otide	\	· ·
	(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO: 57:	\	

22

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	1	
	(2) INFORMATION FOR SEQ ID NO: 58:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	-
10	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:	
15	CTGAAGCTAT GGCTTGCAAT T	
	(2) INFORMATION FOR SEQ ID NO: 59:	·
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:	
	ACAAGTGTCT TCAGATGTTG AT	
30	(2) INFORMATION FOR SEQ ID NO: 60:	
から	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:	
	CTGGATTCTG ACTCACCTTC A	•
45	(2) INFORMATION FOR SEQ ID NO: 61:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	• •
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:	٠.٠
	CCAGGTGAAG TCCTCTGACA	
	·	

(2) INFORMATION FOR SEQ ID NO:62:

5		<b>(</b> .		(A) : (B) : (C) :	NCE ( LENG: TYPE STRAI TOPOI	TH: : : nuc NDEDI	1417 clei NESS	bas c ac : do	e pa id uble	irs	٠							-
10			k) F	EATUI (A) 1	ULE T RE: NAME/ LOCAT	KEY:	: CDS	3	34		٠					<b>.</b>	·	
15		(xi	L) SI	EQUEN	ICE I	ESCF	RIPTI	ON:	SEQ	ip i	NO : 62	2:	-				÷	
	GAG	TTTT	ATA	CCTC	CAATA	GA C	TCTI	CACTA	AG TI	TCT	TTTT	r TC	AGGTT	rgtg	AAA	CTCAAC	2	60
20	TTC	'AAAC	ACA	CTCI	GTTC	CA I	TTC1	GTGG	A CI	ATAA:	GGAI	CAT	CTTI	TAGC	ATCI	GCCGGG	3	120
	TGG	ATGC	CAT	CCAG	GCTT	CT I	TTTC	TACA	T CI	CTGI	TTCI	CG	\TTT1	TGT	GAGO	CTAGG	<b>\</b>	180
	GGT	GCCI	'AAG	CTCC	ATTG	GC T	'CTAG	ATTC	C TG	GCTI	TCÇC	CAI	CATO	TTC	TCCA	AAGCAT	•	240
25	CTG	AAGC	T AI Me	G GC	T TG	C AA	T TG	T CA	G TT	G AT	G CA	G GA	T AC	'A CC	'A CI	C CTC		290
h.				1	- c <sub>j</sub>	2 110	ı Cy	5	.11 116	u Me	c G1		.0	ır Pr	o Le	u Leu		
30	AAG Lys 15	Phe	CCA Pro	TGT Cys	CCA Pro	AGG Arg 20	Leu	AAT Asn	CTT Leu	CTC Leu	TTT Phe 25	vàl	CTG Leu	CTG Leu	ATT	CGT Arg 30		338
35	CTT Leu	TCA Ser	CAA Gln	GTG Val	TCT Ser 35	TCA Ser	GAT Asp	GTT Val	GAT Asp	GAA Glu 40	Gln	CTG Leu	TCC Ser	AAG Lys	TCA Ser 45	GTG Val		386
40	AAA Lys	GAT Asp	AAG Lys	GTA Val 50	TTG Leu	CTG Leu	CCT Pro	TGC Cys	CGT Arg 55	TAC Tyr	AAC Asn	TCT Ser	CCT Pro	CAT His 60	GAA Glu	GAT Asp		434
	GAG Glu	TCT Ser	GAA Glu 65	GAC Asp	CGA Arg	ATC Ile	TAC Tyr	TGG Trp 70	CAA Gln	AAA Lys	CAT His	GAC Asp	AAA Lys 75	GTG Val	GTG Val	CTG Leu		482
45	TCT Ser	GTC Val 80	ATT Ile	GCT Ala	GGG Gly	AAA Lys	CTA Leu 85	AAA Lys	GTG Val	TGG Trp	CCC Pro	GAG Glu 90	TAT Tyr	AAG Lys	AAC Asn	CGG Arg		530
50	ACT Thr 95	TTA Leu	TAT Tyr	GAC Asp	AAC Asn	ACT Thr 100	ACC Thr	TAC Tyr	TCT Ser	CTT Leu	ATC Ile 105	ATC Ile	CTG Leu	GGC Gly	CTG Leu	GTC Val 110		578
55	CTT Leu	TCA Ser	GAC Asp	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	GTC Val 120	GTT Val	CAA Gln	AAG Lys	AAG Lys	GAA Glu 125	AGA Arg	-	<b>62</b> 6
	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	TTA Leu	GTA Val	AAG Lys	TTG Leu	TCC Ser 140	ATC Ile	AAA Lys		 674

	CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly	722
5	145 150 155	
	GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTC ATC ATC Ala Gly Phe Gly Ala Val Ile Thr Val Val Ile Val Val Ile Ile 160 165 170	770
10	AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser 175 180 185 190	818
15	AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala 195 200 205	866
20	GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG Glu Gln Thr Val Phe Leu 210	924
	GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	984
25	ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1044
h	CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1104
	ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1164
30	GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1224
	GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG	1284
35	GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA	1344
	GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG	1404
	AGAGTATTGA GCA	1417
40	(2) INFORMATION FOR SEQ ID NO:63:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 212 amino acids  (B) TYPE: amino acid  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
50 -	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe 1 5 10 15	
55	Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser	

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp

	Lys	Val 50	Leu	Leu	Pro	Cys	Arg 55	Tyr	Asn	Ser	Pro	His 60	Glu	Asp	Glu	Ser	
5	Glu 65	Asp	Arg	Ile	Tyr	Trp 70	Gln	Lys	His	Asp	Lys 75	Val	Val	Leu	Ser	Val	
10	Ile	Ala	Gly	Lys	Leu 85	Lys	Val	Trp	Pro	Glu 90	Tyr	Lys	Asn	Arg	Thr 95	Leu	-
	Tyr	Asp	Asn	Thr 100	Thr	Tyr	Ser	Leu	Ile 105	Ite	Leu	Gly	Leu	Val 110	Leu	Ser	
15	Asp	Arg	Gly 115	Thr	Tyr	Ser	Cys	Val 120	Val	Gln	Lys	Lys	Glu 125	Arg	Gly	Thr	
	Tyr	Glu 130	Val	Lys	His	Leu	Ala 135	Leu	Val	Lys	Leu	Ser 140	Ile	Lys	Pro	Pro	
20	Glu 145	Asp	Pro	Pro	Asp	Ser 150	Lys	Asn	Thr	Leu	va 1	Leu	Phe	Gly	Ala	Gly 160	
25	Phe	Gly	Ala	Val	Ile 165	Thr	Val	Val	Val	Ile 170	Val	Val	Ile	Ile	Lys 175	Cys	
	Phe	Cys	Lys	His 180	Arg	Ser	Cys	Phe	Arg 185	Arg	Asn	Glu	Ala	Ser 190	Arg	Glu	
30	Thr	Asn	Asn 195	Ser	Leu	Thr	Phe	Gly 200	Pro	Glu	Glu	Ala	Leu 205	Ala	Glu	Gln	
	Thr 	Val 210	Phe	Leu													
35	(2)	INFO	RMAT	'ION	FOR	SEQ	ID N	0:64	:								
40		(i)	(A (B (C	) LE ) TY ) ST	E CH NGTH PE: RAND POLO	: 16 nucl EDNE	06 b eic SS:	ase acid doub	pair	s		`					
45					E TY	PE:	cDNA						\		•		
		(1X)		) NA	: ME/KI CATIO								/	\			
50											-			1 .	•		
			•		E DE			-							-		
	GAG I"	ı.ı.LA	TA C	CTCA	ATAG	A CT	CTTA	CTAG	TTT	CTCTT	FTT :	rcago	GTTG:	rg \ai	AACT	CAACC	ė
55	TTCA	AAGA	CA C	TCTG'	TTCC	A TT	rctg:	TGGA	CTA	ATAGO	SAT (	CATC	TTAC	3C Å:	FCTG(	CCGGG	12
	TGGA	rgcc.	AT C	CAGG	CTTC	r TT	TCT	ACAT	CTC'	rgtti	CT (	CGATT	rttt	T d	AGCC	ragga	. 18
														1		AGCAT	24

									1									
	CT	BAAG	CT A'	TG G et A	CT TO la Cy	GC AI ys As	AT TO	ys G	AG T	TG A	TG C	AG G ln A	AT A sp T	CA C	CA C	TC CI	'C	290
5				-				5	1				10	•		•		
. •	AAC Lys	Phe	T CC	A TGT	CCA Pro	A AGG Arg	Lei	AA'. Asi	r CT	r CT	C TT u Phe	e Vai	G CT	G CT u Le	G AT u Il	T CGT e Arg 30		338
10	CTI Lev	TC/	A CAZ	A GTO	TCI Ser	Ser	GAT Asp	GTT Val	GAT L Asp	GAZ Glu	A CAM u Gli	A CTO	G TC	C AA	G TC s Se 4	A GTG r Val 5		386
15	AAA Lys	GAT Asp	T AAG D Lys	GTA Val	Leu	CTG Leu	CCT	TGC Cys	C CGI Arg	Туг	AAC	TCT Ser	CC:	CA' His	s Gl	A GAT u Asp		434
20	GAG Glu	TC1 Ser	GAA Glu 65	Asp	CGA Arg	ATC	TAC	TGG Trp	Gln	AAA Lys	CAT His	GAC Asp	AAA Lys	Va]	G GTO	G CTG L Leu	•	182
25	ser	80	ııe	Ala	GIA	Lys	Leu 85	Lys	Val	Trp	Pro	Ġlu  90 	Туг	Lys	s Asr	C CGG n Arg	9	30
	ACT Thr 95	TTA Leu	TAT Tyr	GAC Asp	AAC Asn	ACT Thr 100	ACC Thr	TAC Tyr	TCT Ser	CTT Leu	ATC Ile 105	ΙΙ¢	CTG Leu	GGC	CTC Leu	GTC Val		78
b <sup>30</sup>	CTT Leu	TCA Ser	GAC Asp	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	GTC Val 120	GTT Val	CAA Gln	AAG Lys	AAG Lys	GAA Glu _125	AGA Arg	6	26
35	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	TTA Leu	GTA Val	ÄÄG Lys	TTG Leu	TCC Ser	Ile	AAA Lys	. 6	74
40	CCC Pro	CCA Pro	GAA Glu 145	GAC Asp	CCT Pro	CCT Pro	GAT Asp	AGC Ser 150	AAG Lys	AAC Asn	ACA Thr	CTT Leu	GTG Val 155	CTC	TTT Phe	GGG Gly	7	22
45	GCA Ala	GGA Gly 160	TTC Phe	GGC Gly	GCA Ala	GTA Val	ATA Ile 165	ACA Thr	GTC Val	GTC Val	GTC Val	ATC Ile 170	GTT Val	GTC Vall	ATC Ile	ATC Ile	7	70
,5	AAA Lys 175	TGC Cys	TTC Phe	TGT Cys	AAG Lys	CAC His 180	GGT Gly	CTC Leu	ATC Ile	TAC Tyr	CAT His 185	TTG Leu	CAA Gln	CTG Leu	ACC Thr	TCT Ser 190	8:	18
50	TCT	GCA Ala	AAG Lys	GAC Asp	TTC Phe 195	AGA Arg	AAC Asn	CTA Leu	GCA Ala	CTA Leu 200	CCC Pro	TGG Trp	CTC Leu	TGC Cys	AAA Lys 205	CAC His	86	56
55	GGT Gly	TCT Ser	Leu	GGT Gly 210	GAA Glu	GCC Ala	TCT Ser	Ala	GTG Val 215	ATT Ile	TGC Cys	AGA Arg	AGT Ser	ACT Thr 220		ACG Thr	- 91	Ĺ <b>4</b>

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_	ρ - 95 - _	•
AAT GAA CCA CAG TAGTTCTGCT GT Asn Glu Pro Gln 225	TTCTGAGG ACGTAGTTTA GAGACTGAAT	966
50		
TCTTTGGAAA GGACATAGGG ACAGTTT	GCA CATTTGCTTG CACATCACAC ACACACACAC	1026
•	CAC ACACACAC ACACACAC TCTCTCTCTC	1086
	TTC TACCCTGTTG CTCAGTGACA AAGAATCACT	1146
	CAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC	1206
	TAG CAGAACACTA GCTGAATCAA TGAAGACACT	1266
	GAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT	1326
•	CCC AAGCTCTGAG CTCATAGACA AGCTAATTTA	1386
	AGT TAGTACGGGG TTCAGGATAC TGCTTACTGG	1446
•	IGT TTTTTAAAGG CCTACTGACT GTAGTGTAAT	1506
TTGTAGGAAA CATGTTGCTA TGTATACC	CCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT	1566
CAGCCAGCAC TTTCCAGGTA TTTCCCTT	TTT TATCCTTCAT	1606
(2) INFORMATION FOR SEQ ID NO:	:65:	
(i) SEQUENCE CHARACTERI  (A) LENGTH: 226 a  (B) TYPE: amino a  (D) TOPOLOGY: lin	mino acids \	
(ii) MOLECULE TYPE: prot	ein	
(xi) SEQUENÇE DESCRIPTIO	N: SEQ ID NO:65:	
Met Ala Cys Asn Cys Gln Leu Me 1 5	t Gln Asp Thr Pro Leu Leu Lys Phe	

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp 

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser 

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val 

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu 

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser 

- 96 -Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr 120 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro 5 135 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly 155 160 10 Phe Gly Ala Val Ile Thr Val Val Val Val Val Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala 180 185 15 Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp L $^{\prime}_{
m c}$ u Cys Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu 20 215 **À**20

Pro Gln 225